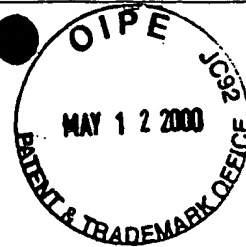


SEQUENCE LISTING



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<110> Marks, James D

Poul, Marie A

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<140> 09/250,056

<141> 1999-02-12

<150> 60/082,953

<151> 1998-04-24

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acid sequence

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B3
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1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Arg Gly Asp Asn Thr Tyr Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys Met Thr Ser Asn Ala Phe Ala Phe Asp Tyr Trp Gly Gln Gly

100

105

110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

115

120

125

Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val

130

135

140

Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser Ser
145 150 155 160

Ser Asn Ile Gly Ala Gly Tyr Gly Val His Trp Tyr Gln Gln Leu Pro
165 170 175

Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asn Thr Asn Arg Pro Ser
180 185 190

Gly Val Pro Asp Arg Phe Ser Gly Phe Lys Ser Gly Thr Ser Ala Ser
195 200 205

Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
210 215 220

Gln Phe Tyr Asp Ser Ser Leu Ser Gly Trp Val Phe Gly Gly Gly Thr
225 230 235 240

Lys Leu Thr Val Leu Gly
245

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<222> (223) .. (231)

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

B3
21
Ser Ser Ile Ser Gly Ser Ser Arg Tyr Ile Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Met Asp Ala Ser Gly Ser Tyr Phe Asn Phe Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Glu Thr Thr Leu Thr Gln Ser Pro Ser Phe
130 135 140

Leu Ser Ala Phe Val Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser
145 150 155 160

Pro Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
165 170 175

Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val
180 185 190

B3
wf Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asn Ser Tyr Pro Leu Ser Phe Gly Gly Gly Thr Lys Val Glu Ile
225 230 235 240

Lys Arg

<210> 3

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encoding scFv F5 Ab

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ccagggaagg ggctggagtg ggtctcagct attagtggtc gtggtgataa cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
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agtaacgcgt tcgcatttga ctactggggc cagggaaccc tggtcaccgt ctctcagggt 360
ggaggcggtt caggcggagg tggctctggc ggtggcggat cgcagtctgt gttgacgcag 420
ccgccctcag tgtctggggc cccagggcag agggtcacca tctcctgcac tgggagcagc 480
tccaacatcg gggcagggtta tgggtgtacac tgggtaccagc agcttccagg aacagccccc 540
aaactcctca tctatggtaa caccaatcgg ccctcagggg tccctgaccg attctctggc 600
ttcaagtctg gcacctcagc ctccctggcc atcactgggc tccaggctga ggatgaggct 660
gattattact gccagttcta tgacagcagc ctgagtgggt ggggtgttcgg cggagggacc 720
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encoding scFv C1 amino acid sequence

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<221> modified_base

<222> (111)

<223> N = A, C, G, OR T

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B³
21

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tcctgtgcag cctctggatt caccttttagc agctatgccca tgggctgggt ncgccaggct 120
ccagggaagg ggctggagtg ggtctcatca attagtggca gtagtagata catatattac 180
gcagactccg tgaagggccg gttcaccatc tcccagagaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgag agccgaggac acggccggtt attactgtgc gaaaatggat 300
gcttcgggga gttattttta tttctggggc cagggcaccc tggtcaccgt ctctcaggt 360
ggaggcgggt caggcggagg tggctctggc ggtggcggat cggaaacgac actcacgcag 420
tctccatcct tcctgtctgc attttagga gacagaatca ccatcacttg ccgggccagt 480
ccgggcatta ggaattatct agcctggtat cagcaaaaac cagggaagc ccctaagctc 540
ctgatctatg ctgcatctac tttgcaaagt ggggtcccat caagggttcag cggcagtggg 600
tctgggacag attttactct caccatcagc agcctgcagc ctgaagattt tgcaacttat 660
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Arg Glu Asp Leu Lys

1 5

<210> 6

<211> 4

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B3
wf
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<223> Description of Artificial Sequence:: translocation
sequence

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Arg Glu Asp Leu

1

<210> 7

<211> 4

<212> PRT

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<223> Description of Artificial Sequence:: translocation
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Arg Asp Glu Leu

1

<210> 8

B3
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Lys Asp Glu Leu

1
